

Figure 1.
(a) Nucleotide sequences for Ala-Ile-Lys-Leu-Val-Gln-Ser-Pro and showing codon frequencies in relation to usage in enteric bacterial genes

Ala	Ile	Lys	Leu	Val	Gln	Ser
GCU 0.35	AUC 0.83	AAA 0.74	CUG 0.83	GUU 0.51	CAG 0.86	UCC 0.37
GCA 0.28	AUU 0.17	AAG 0.26	CUC 0.07	GUA 0.26	CAA 0.14	UCU 0.34
GCG 0.26	AUA 0.00		CUU 0.04	GUG 0.16		AGC 0.20
GCC 0.10			UUG 0.03	GUC 0.07		UCG 0.04
			UUA 0.02			AGU 0.03
			CUA 0.00			UCA 0.02
178	260	269	135	125	230	158

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Pro

CCG 0.77
CCA 0.15
CCU 0.08
CCC 0.00

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(b) Nucleotide sequences for Ala-Ile-Lys-Leu-Val-Gln-Ser-Pro-Asn-Gly-Asn-Phe-Ala-Ala-Ser and showing codon frequencies in relation to usage in enteric bacterial genes

Ala	Ile	Lys	Leu	Val	Gln	Ser
GCU 0.35	AUC 0.83	AAA 0.74	CUG 0.83	GUU 0.51	CAG 0.86	UCC 0.37
GCA 0.28	AUU 0.17	AAG 0.26	CUC 0.07	GUA 0.26	CAA 0.14	UCU 0.34
GCG 0.26	AUA 0.00		CUU 0.04	GUG 0.16		AGC 0.20
GCC 0.10			UUG 0.03	GUC 0.07		UCG 0.04
			UUA 0.02			AGU 0.03
			CUA 0.00			UCA 0.02
178	260	269	135	125	230	158

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Pro	Asn	Gly	Asn	Phe	Ala	Ala
CCG 0.77	AAC 0.94	GGU 0.59	AAC 0.94	UUC 0.76	GCU 0.35	GCU 0.35
CCA 0.15	AAU 0.06	GGC 0.38	AAU 0.06	UUU 0.24	GCA 0.28	GCA 0.28
CCU 0.08		GGG 0.02			GCG 0.26	GCG 0.26
CCC 0.00		GGA 0.00			GCC 0.10	GCC 0.10
401	396	148	88	34	34	50

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Ser

UCC 0.37
UCU 0.34
AGC 0.20
UCG 0.04
AGU 0.03
UCA 0.02
119

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(c) Nucleotide sequences for Ala-Ile-Lys-Leu-Val-Gln-Ser-Pro-Asn-Gly-Asn-Phe-Ala-Ser-Phe-Val-Leu-Asp-Gly-Thr-Lys-Trp-Ile-Phe-Lys-Ser-Lys-Tyr-Tyr and showing codon frequencies in relation to usage in enteric bacterial genes.

Ala	Ile	Lys	Leu	Val	Gln	Ser
GCU 0.35	AUC 0.83	AAA 0.74	CUG 0.83	GUU 0.51	CAG 0.86	UCC 0.37
GCA 0.28	AUU 0.17	AAG 0.26	CUC 0.07	GUA 0.26	CAA 0.14	UCU 0.34
GCG 0.26	AUA 0.00		CUU 0.04	GUG 0.16		AGC 0.20
GCC 0.10			UUG 0.03	GUC 0.07		UCG 0.04
			UUA 0.02			AGU 0.03
			CUA 0.00			UCA 0.02
178	260	269	135	125	230	158

Pro	Asn	Gly	Asn	Phe	Ala	Ala
CCG 0.77	AAC 0.94	GGU 0.59	AAC 0.94	UUC 0.76	GCU 0.35	GCU 0.35
CCA 0.15	AAU 0.06	GGC 0.38	AAU 0.06	UUU 0.24	GCA 0.28	GCA 0.28
CCU 0.08		GGG 0.02			GCG 0.26	GCG 0.26
CCC 0.00		GGA 0.00			GCC 0.10	GCC 0.10
401	396	148	88	34	34	50

Ser	Phe	Val	Leu	Asp	Gly	Thr
UCC 0.37	UUC 0.76	GUU 0.51	CUG 0.83	GAC 0.67	GGU 0.59	ACC 0.55
UCU 0.34	UUU 0.24	GUA 0.26	CUC 0.07	GAU 0.33	GGC 0.38	ACU 0.35
AGC 0.20		GUG 0.16	CUU 0.04		GGG 0.02	ACG 0.07
UCG 0.04		GUC 0.07	UUG 0.03		GGA 0.00	ACA 0.04
AGU 0.03			UUA 0.02			
UCA 0.02			CUA 0.00			
119	216	167	180	161	240	338

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22 - 28		Trp		Ile		Phe		Lys		Ser		Lys	
Lys													
AAA 0.74		UGG 1.00		AUC 0.83		UUC 0.76		AAA 0.74		UCC 0.37		AAA 0.74	
AAG 0.26				AUU 0.17		UUU 0.24		AAG 0.26		UCU 0.34		AAG 0.26	
				AUA 0.00						AGC 0.20			
										UCG 0.04			
										AGU 0.03			
										UCA 0.02			
467		467		173		154		152		154		0	
29 - 30		Tyr											
Tyr													
UAC 0.75		UAC 0.75											
UAU 0.25		UAU 0.25											
0		0											